

amdtE

SEQUENCE LISTING

T, 6570
<110> EVANS, RONALD M.
NO, DAVID
SAEZ, ENRIQUE

<120> METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO

<130> SALK1520-2

<140> 09/042,488

<141> 1998-03-16

D
<150> 08/974,530

<151> 1997-11-19

<150> 08/628,830

<151> 1996-04-05

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 71

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
peptide sequence

<220>

<221> MOD_RES

<222> (2)..(3)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (5)..(6)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (8)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (10)

<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(17)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (19)..(20)
<223> Any amino acid

E
<220>
<221> MOD_RES
<222> (23)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (26)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (28)..(38)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (40)..(47)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (49)..(51)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (53)..(54)
<223> Amny amino acid

<220>
<221> MOD_RES
<222> (56)..(57)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (59)..(60)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (63)..(64)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (67)..(69)
<223> Any amino acid

<400> 1
Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
1 5 10 15
Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
35 40 45
Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
50 55 60
Lys Cys Xaa Xaa Xaa Gly Met
65 70

<210> 2
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2
Glu Gly Cys Lys Gly
1 5

<210> 3
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 3
 Gly Ser Cys Lys Val
 1 5

<210> 4
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Recombinant VgEcR

<220>
 <221> CDS
 <222> (1)..(2238)

<400> 4
 atg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac 48
 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15

 ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 96
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

 ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 144
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

 cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 192
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

 gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag 240
 Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
 65 70 75 80

 ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc 288
 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa	336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu	
100 105 110	
agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa	384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln	
115 120 125	
gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac	432
Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr	
130 135 140	
aac gcc ctc acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt	480
Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val	
145 150 155 160	
acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg	528
Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met	
165 170 175	
gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc	576
Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys	
180 185 190	
ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt	624
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys	
195 200 205	
gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg	672
Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met	
210 215 220	
acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct	720
Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser	
225 230 235 240	
ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca	768
Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr	
245 250 255	
tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata	816
Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile	
260 265 270	
ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag	864
Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln	
275 280 285	
ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag	912
Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln	
290 295 300	

cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac	960
Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn	
305 310 315 320	
gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata	1008
Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile	
325 330 335	
ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt	1056
Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe	
340 345 350	
aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg	1104
Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser	
355 360 365	
tcg gag gtg atg atg ctg cgt atg gca cga cgc tat gac cac agc tcg	1152
Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser	
370 375 380	
gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac	1200
Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr	
385 390 395 400	
aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc	1248
Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys	
405 410 415	
cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc	1296
Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu	
420 425 430	
act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa	1344
Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln	
435 440 445	
cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat	1392
Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr	
450 455 460	
ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca	1440
Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala	
465 470 475 480	
aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac	1488
Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn	
485 490 495	
gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag	1536
Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys	
500 505 510	

E

ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag	1584
Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln	
515 520 525	
tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct	1632
Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala	
530 535 540	
gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat	1680
Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp	
545 550 555 560	
tgc gac tct gcc tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag	1728
Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln	
565 570 575	
cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat	1776
Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp	
580 585 590	
tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag	1824
Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln	
595 600 605	
ctg caa ggt caa ctg caa ccc cag ctc caa cca cag ctt cag acg caa	1872
Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln	
610 615 620	
ctc cag cca cag att caa cca cag cca cag ctc ctt ccc gtc tcc gct	1920
Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala	
625 630 635 640	
ccc gtg ccc gcc tcc gta acc gca cct ggt tcc ttg tcc gcg gtc agt	1968
Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser	
645 650 655	
acg agc agc gaa tac atg ggc gga agt gcg gcc ata gga ccc atc acg	2016
Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr	
660 665 670	
ccg gca acc acc agc agt atc acg gct gcc gtt acc gct agc tcc acc	2064
Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr	
675 680 685	
aca tca gcg gta ccg atg ggc aac gga gtt gga gtc ggt gtt ggg gtg	2112
Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val	
690 695 700	
ggc ggc aac gtc agc atg tat gcg aac gcc cag acg gcg atg gcc ttg	2160
Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu	
705 710 715 720	

E

atg ggt gta gcc ctg cat tcg cac caa gag cag ctt atc ggg gga gtg 2208
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

gcg gtt aag tcg gag cac tcg acg act gca tag 2241
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

<210> 5
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Recombinant
 VgEcR

<400> 5
 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

E

Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	180	185	190
Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Asn	Gln	Cys	195	200	205
Ala	Met	Lys	Arg	Arg	Glu	Lys	Lys	Ala	Gln	Lys	Glu	Lys	Asp	Lys	Met	210	215	220
Thr	Thr	Ser	Pro	Ser	Ser	Gln	His	Gly	Gly	Asn	Gly	Ser	Leu	Ala	Ser	225	230	235
Gly	Gly	Gly	Gln	Asp	Phe	Val	Lys	Lys	Glu	Ile	Leu	Asp	Leu	Met	Thr	245	250	255
Cys	Glu	Pro	Pro	Gln	His	Ala	Thr	Ile	Pro	Leu	Leu	Pro	Asp	Glu	Ile	260	265	270
Leu	Ala	Lys	Cys	Gln	Ala	Arg	Asn	Ile	Pro	Ser	Leu	Thr	Tyr	Asn	Gln	275	280	285
Leu	Ala	Val	Ile	Tyr	Lys	Leu	Ile	Trp	Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	290	295	300
Pro	Ser	Glu	Glu	Asp	Leu	Arg	Arg	Ile	Met	Ser	Gln	Pro	Asp	Glu	Asn	305	310	315
Glu	Ser	Gln	Thr	Asp	Val	Ser	Phe	Arg	His	Ile	Thr	Glu	Ile	Thr	Ile	325	330	335
Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe	340	345	350
Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	355	360	365
Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	Arg	Arg	Tyr	Asp	His	Ser	Ser	370	375	380
Asp	Ser	Ile	Phe	Phe	Ala	Asn	Asn	Arg	Ser	Tyr	Thr	Arg	Asp	Ser	Tyr	385	390	395
Lys	Met	Ala	Gly	Met	Ala	Asp	Asn	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	405	410	415
Arg	Gln	Met	Phe	Ser	Met	Lys	Val	Asp	Asn	Val	Glu	Tyr	Ala	Leu	Leu	420	425	430
Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	Pro	Gly	Leu	Glu	Lys	Ala	Gln	435	440	445

Leu	Val	Glu	Ala	Ile	Gln	Ser	Tyr	Tyr	Ile	Asp	Thr	Leu	Arg	Ile	Tyr
450						455					460				
Ile	Leu	Asn	Arg	His	Cys	Gly	Asp	Ser	Met	Ser	Leu	Val	Phe	Tyr	Ala
465					470					475					480
Lys	Leu	Leu	Ser	Ile	Leu	Thr	Glu	Leu	Arg	Thr	Leu	Gly	Asn	Gln	Asn
				485					490					495	
Ala	Glu	Met	Cys	Phe	Ser	Leu	Lys	Leu	Lys	Asn	Arg	Lys	Leu	Pro	Lys
			500					505					510		
Phe	Leu	Glu	Glu	Ile	Trp	Asp	Val	His	Ala	Ile	Pro	Pro	Ser	Val	Gln
		515					520					525			
Ser	His	Leu	Gln	Ile	Thr	Gln	Glu	Glu	Asn	Glu	Arg	Leu	Glu	Arg	Ala
	530					535					540				
Glu	Arg	Met	Arg	Ala	Ser	Val	Gly	Gly	Ala	Ile	Thr	Ala	Gly	Ile	Asp
545					550					555					560
Cys	Asp	Ser	Ala	Ser	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Gln	His	Gln
				565					570					575	
Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Ser	Ser	Leu	Thr	Gln	Asn	Asp
			580					585					590		
Ser	Gln	His	Gln	Thr	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Pro	Pro	Gln
		595					600					605			
Leu	Gln	Gly	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Thr	Gln
	610					615					620				
Leu	Gln	Pro	Gln	Ile	Gln	Pro	Gln	Pro	Gln	Leu	Leu	Pro	Val	Ser	Ala
625					630					635					640
Pro	Val	Pro	Ala	Ser	Val	Thr	Ala	Pro	Gly	Ser	Leu	Ser	Ala	Val	Ser
				645					650					655	
Thr	Ser	Ser	Glu	Tyr	Met	Gly	Gly	Ser	Ala	Ala	Ile	Gly	Pro	Ile	Thr
			660					665					670		
Pro	Ala	Thr	Thr	Ser	Ser	Ile	Thr	Ala	Ala	Val	Thr	Ala	Ser	Ser	Thr
		675					680					685			
Thr	Ser	Ala	Val	Pro	Met	Gly	Asn	Gly	Val	Gly	Val	Gly	Val	Gly	Val
	690					695					700				
Gly	Gly	Asn	Val	Ser	Met	Tyr	Ala	Asn	Ala	Gln	Thr	Ala	Met	Ala	Leu
705					710					715					720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
725 730 735

Ala Val Lys Ser Glu His Ser Thr Thr Ala
740 745

<210> 6
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Recombinant
VpEcR

<220>
<221> CDS
<222> (1)..(2238)

<400> 6
atg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac 48
Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
1 5 10 15
ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 96
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
20 25 30
ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 144
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
35 40 45
cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 192
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
50 55 60
gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag 240
Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
65 70 75 80
ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc 288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
85 90 95
gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa 336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
100 105 110
agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa 384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
115 120 125

gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac	432
Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr	
130 135 140	
aac gcc ctc acc tgt gag ggc tgc aag ggg ttc ttt cga cgc agc gtt	480
Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val	
145 150 155 160	
acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg	528
Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met	
165 170 175	
gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc	576
Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys	
180 185 190	
ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt	624
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys	
195 200 205	
gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg	672
Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met	
210 215 220	
acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct	720
Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser	
225 230 235 240	
ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca	768
Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr	
245 250 255	
tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata	816
Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile	
260 265 270	
ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag	864
Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln	
275 280 285	
ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag	912
Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln	
290 295 300	
cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac	960
Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn	
305 310 315 320	
gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata	1008
Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile	
325 330 335	

E

ctc	acg	gtc	cag	ttg	att	gtt	gag	ttt	gct	aaa	ggt	cta	cca	gcg	ttt	1056
Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe	
			340					345					350			
aca	aag	ata	ccc	cag	gag	gac	cag	atc	acg	tta	cta	aag	gcc	tgc	tcg	1104
Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	
		355					360					365				
tcg	gag	gtg	atg	atg	ctg	cgt	atg	gca	cga	cgc	tat	gac	cac	agc	tcg	1152
Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	Arg	Arg	Tyr	Asp	His	Ser	Ser	
	370					375					380					
gac	tca	ata	ttc	ttc	gcg	aat	aat	aga	tca	tat	acg	cgg	gat	tct	tac	1200
Asp	Ser	Ile	Phe	Phe	Ala	Asn	Asn	Arg	Ser	Tyr	Thr	Arg	Asp	Ser	Tyr	
385					390					395					400	
aaa	atg	gcc	gga	atg	gct	gat	aac	att	gaa	gac	ctg	ctg	cat	ttc	tgc	1248
Lys	Met	Ala	Gly	Met	Ala	Asp	Asn	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	
			405					410						415		
cgc	caa	atg	ttc	tcg	atg	aag	gtg	gac	aac	gtc	gaa	tac	gcg	ctt	ctc	1296
Arg	Gln	Met	Phe	Ser	Met	Lys	Val	Asp	Asn	Val	Glu	Tyr	Ala	Leu	Leu	
			420					425					430			
act	gcc	att	gtg	atc	ttc	tcg	gac	cgg	ccg	ggc	ctg	gag	aag	gcc	caa	1344
Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	Pro	Gly	Leu	Glu	Lys	Ala	Gln	
		435					440					445				
cta	gtc	gaa	gcg	atc	cag	agc	tac	tac	atc	gac	acg	cta	cgc	att	tat	1392
Leu	Val	Glu	Ala	Ile	Gln	Ser	Tyr	Tyr	Ile	Asp	Thr	Leu	Arg	Ile	Tyr	
	450					455					460					
ata	ctc	aac	cgc	cac	tgc	ggc	gac	tca	atg	agc	ctc	gtc	ttc	tac	gca	1440
Ile	Leu	Asn	Arg	His	Cys	Gly	Asp	Ser	Met	Ser	Leu	Val	Phe	Tyr	Ala	
465					470					475					480	
aag	ctg	ctc	tcg	atc	ctc	acc	gag	ctg	cgt	acg	ctg	ggc	aac	cag	aac	1488
Lys	Leu	Leu	Ser	Ile	Leu	Thr	Glu	Leu	Arg	Thr	Leu	Gly	Asn	Gln	Asn	
				485					490					495		
gcc	gag	atg	tgt	ttc	tca	cta	aag	ctc	aaa	aac	cgc	aaa	ctg	ccc	aag	1536
Ala	Glu	Met	Cys	Phe	Ser	Leu	Lys	Leu	Lys	Asn	Arg	Lys	Leu	Pro	Lys	
			500					505					510			
ttc	ctc	gag	gag	atc	tgg	gac	gtt	cat	gcc	atc	ccg	cca	tcg	gtc	cag	1584
Phe	Leu	Glu	Glu	Ile	Trp	Asp	Val	His	Ala	Ile	Pro	Pro	Ser	Val	Gln	
		515					520					525				
tcg	cac	ctt	cag	att	acc	cag	gag	gag	aac	gag	cgt	ctc	gag	cgg	gct	1632
Ser	His	Leu	Gln	Ile	Thr	Gln	Glu	Glu	Asn	Glu	Arg	Leu	Glu	Arg	Ala	
	530					535					540					

E

gag	cgt	atg	cgg	gca	tcg	gtt	ggg	ggc	gcc	att	acc	gcc	ggc	att	gat	1680
Glu	Arg	Met	Arg	Ala	Ser	Val	Gly	Gly	Ala	Ile	Thr	Ala	Gly	Ile	Asp	
545					550					555					560	
tgc	gac	tct	gcc	tcc	act	tcg	gcg	gcg	gca	gcc	gcg	gcc	cag	cat	cag	1728
Cys	Asp	Ser	Ala	Ser	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Gln	His	Gln	
				565					570					575		
cct	cag	cct	cag	ccc	cag	ccc	caa	ccc	tcc	tcc	ctg	acc	cag	aac	gat	1776
Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Ser	Ser	Leu	Thr	Gln	Asn	Asp	
			580					585					590			
tcc	cag	cac	cag	aca	cag	ccg	cag	cta	caa	cct	cag	cta	cca	cct	cag	1824
Ser	Gln	His	Gln	Thr	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Pro	Pro	Gln	
		595					600					605				
ctg	caa	ggt	caa	ctg	caa	ccc	cag	ctc	caa	cca	cag	ctt	cag	acg	caa	1872
Leu	Gln	Gly	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Thr	Gln	
	610					615					620					
ctc	cag	cca	cag	att	caa	cca	cag	cca	cag	ctc	ctt	ccc	gtc	tcc	gct	1920
Leu	Gln	Pro	Gln	Ile	Gln	Pro	Gln	Pro	Gln	Leu	Leu	Pro	Val	Ser	Ala	
625					630					635					640	
ccc	gtg	ccc	gcc	tcc	gta	acc	gca	cct	ggt	tcc	ttg	tcc	gcg	gtc	agt	1968
Pro	Val	Pro	Ala	Ser	Val	Thr	Ala	Pro	Gly	Ser	Leu	Ser	Ala	Val	Ser	
				645					650					655		
acg	agc	agc	gaa	tac	atg	ggc	gga	agt	gcg	gcc	ata	gga	ccc	atc	acg	2016
Thr	Ser	Ser	Glu	Tyr	Met	Gly	Gly	Ser	Ala	Ala	Ile	Gly	Pro	Ile	Thr	
			660					665					670			
ccg	gca	acc	acc	agc	agt	atc	acg	gct	gcc	gtt	acc	gct	agc	tcc	acc	2064
Pro	Ala	Thr	Thr	Ser	Ser	Ile	Thr	Ala	Ala	Val	Thr	Ala	Ser	Ser	Thr	
		675					680					685				
aca	tca	gcg	gta	ccg	atg	ggc	aac	gga	gtt	gga	gtc	ggt	gtt	ggg	gtg	2112
Thr	Ser	Ala	Val	Pro	Met	Gly	Asn	Gly	Val	Gly	Val	Gly	Val	Gly	Val	
	690					695					700					
ggc	ggc	aac	gtc	agc	atg	tat	gcg	aac	gcc	cag	acg	gcg	atg	gcc	ttg	2160
Gly	Gly	Asn	Val	Ser	Met	Tyr	Ala	Asn	Ala	Gln	Thr	Ala	Met	Ala	Leu	
705					710					715					720	
atg	ggt	gta	gcc	ctg	cat	tcg	cac	caa	gag	cag	ctt	atc	ggg	gga	gtg	2208
Met	Gly	Val	Ala	Leu	His	Ser	His	Gln	Glu	Gln	Leu	Ile	Gly	Gly	Val	
				725					730					735		
gcg	gtt	aag	tcg	gag	cac	tcg	acg	act	gca	tag						2241
Ala	Val	Lys	Ser	Glu	His	Ser	Thr	Thr	Ala							
			740					745								

<210> 7
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
 VpEcr

<400> 7

Met	Ala	Pro	Pro	Thr	Asp	Val	Ser	Leu	Gly	Asp	Glu	Leu	His	Leu	Asp	1	5	10	15
Gly	Glu	Asp	Val	Ala	Met	Ala	His	Ala	Asp	Ala	Leu	Asp	Asp	Phe	Asp	20	25	30	
Leu	Asp	Met	Leu	Gly	Asp	Gly	Asp	Ser	Pro	Gly	Pro	Gly	Phe	Thr	Pro	35	40	45	
His	Asp	Ser	Ala	Pro	Tyr	Gly	Ala	Leu	Asp	Met	Ala	Asp	Phe	Glu	Phe	50	55	60	
Glu	Gln	Met	Phe	Thr	Asp	Ala	Leu	Gly	Ile	Asp	Glu	Tyr	Gly	Gly	Lys	65	70	75	80
Leu	Leu	Gly	Thr	Ser	Arg	Arg	Ile	Ser	Asn	Ser	Ile	Ser	Ser	Gly	Arg	85	90	95	
Asp	Asp	Leu	Ser	Pro	Ser	Ser	Ser	Leu	Asn	Gly	Tyr	Ser	Ala	Asn	Glu	100	105	110	
Ser	Cys	Asp	Ala	Lys	Lys	Ser	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Val	Gln	115	120	125	
Glu	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	130	135	140	
Asn	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	145	150	155	160
Thr	Lys	Ser	Ala	Val	Tyr	Cys	Cys	Lys	Phe	Gly	Arg	Ala	Cys	Glu	Met	165	170	175	
Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	180	185	190	
Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Asn	Gln	Cys	195	200	205	
Ala	Met	Lys	Arg	Arg	Glu	Lys	Lys	Ala	Gln	Lys	Glu	Lys	Asp	Lys	Met	210	215	220	

Thr	Thr	Ser	Pro	Ser	Ser	Gln	His	Gly	Gly	Asn	Gly	Ser	Leu	Ala	Ser		
225					230					235					240		
Gly	Gly	Gly	Gln	Asp	Phe	Val	Lys	Lys	Glu	Ile	Leu	Asp	Leu	Met	Thr		
				245					250					255			
Cys	Glu	Pro	Pro	Gln	His	Ala	Thr	Ile	Pro	Leu	Leu	Pro	Asp	Glu	Ile		
			260					265					270				
Leu	Ala	Lys	Cys	Gln	Ala	Arg	Asn	Ile	Pro	Ser	Leu	Thr	Tyr	Asn	Gln		
		275					280					285					
Leu	Ala	Val	Ile	Tyr	Lys	Leu	Ile	Trp	Tyr	Gln	Asp	Gly	Tyr	Glu	Gln		
		290				295					300						
Pro	Ser	Glu	Glu	Asp	Leu	Arg	Arg	Ile	Met	Ser	Gln	Pro	Asp	Glu	Asn		
305					310					315					320		
Glu	Ser	Gln	Thr	Asp	Val	Ser	Phe	Arg	His	Ile	Thr	Glu	Ile	Thr	Ile		
				325					330					335			
Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe		
			340					345					350				
Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser		
		355					360					365					
Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	Arg	Arg	Tyr	Asp	His	Ser	Ser		
		370				375					380						
Asp	Ser	Ile	Phe	Phe	Ala	Asn	Asn	Arg	Ser	Tyr	Thr	Arg	Asp	Ser	Tyr		
385					390					395					400		
Lys	Met	Ala	Gly	Met	Ala	Asp	Asn	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys		
				405					410					415			
Arg	Gln	Met	Phe	Ser	Met	Lys	Val	Asp	Asn	Val	Glu	Tyr	Ala	Leu	Leu		
			420					425					430				
Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	Pro	Gly	Leu	Glu	Lys	Ala	Gln		
		435					440					445					
Leu	Val	Glu	Ala	Ile	Gln	Ser	Tyr	Tyr	Ile	Asp	Thr	Leu	Arg	Ile	Tyr		
		450				455					460						
Ile	Leu	Asn	Arg	His	Cys	Gly	Asp	Ser	Met	Ser	Leu	Val	Phe	Tyr	Ala		
465					470					475					480		
Lys	Leu	Leu	Ser	Ile	Leu	Thr	Glu	Leu	Arg	Thr	Leu	Gly	Asn	Gln	Asn		
				485					490					495			

Ala	Glu	Met	Cys	Phe	Ser	Leu	Lys	Leu	Lys	Asn	Arg	Lys	Leu	Pro	Lys		
			500						505					510			
Phe	Leu	Glu	Glu	Ile	Trp	Asp	Val	His	Ala	Ile	Pro	Pro	Ser	Val	Gln		
		515					520					525					
Ser	His	Leu	Gln	Ile	Thr	Gln	Glu	Glu	Asn	Glu	Arg	Leu	Glu	Arg	Ala		
	530					535					540						
Glu	Arg	Met	Arg	Ala	Ser	Val	Gly	Gly	Ala	Ile	Thr	Ala	Gly	Ile	Asp		
545					550					555					560		
Cys	Asp	Ser	Ala	Ser	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Gln	His	Gln		
				565					570					575			
Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Ser	Ser	Leu	Thr	Gln	Asn	Asp		
			580					585					590				
Ser	Gln	His	Gln	Thr	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Pro	Pro	Gln		
		595					600					605					
Leu	Gln	Gly	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Thr	Gln		
	610					615					620						
Leu	Gln	Pro	Gln	Ile	Gln	Pro	Gln	Pro	Gln	Leu	Leu	Pro	Val	Ser	Ala		
625					630					635					640		
Pro	Val	Pro	Ala	Ser	Val	Thr	Ala	Pro	Gly	Ser	Leu	Ser	Ala	Val	Ser		
				645					650					655			
Thr	Ser	Ser	Glu	Tyr	Met	Gly	Gly	Ser	Ala	Ala	Ile	Gly	Pro	Ile	Thr		
			660					665					670				
Pro	Ala	Thr	Thr	Ser	Ser	Ile	Thr	Ala	Ala	Val	Thr	Ala	Ser	Ser	Thr		
		675					680					685					
Thr	Ser	Ala	Val	Pro	Met	Gly	Asn	Gly	Val	Gly	Val	Gly	Val	Gly	Val		
	690					695					700						
Gly	Gly	Asn	Val	Ser	Met	Tyr	Ala	Asn	Ala	Gln	Thr	Ala	Met	Ala	Leu		
705					710					715					720		
Met	Gly	Val	Ala	Leu	His	Ser	His	Gln	Glu	Gln	Leu	Ile	Gly	Gly	Val		
				725					730					735			
Ala	Val	Lys	Ser	Glu	His	Ser	Thr	Thr	Ala								
			740					745									

<210> 8
 <211> 3126
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
 GEcR

<220>

<221> CDS

<222> (1)..(3123)

<400> 8

atg gac tcc aaa gaa tca tta act cct ggt aga gaa gaa aac ccc agc	48
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser	
1 5 10 15	
agt gtg ctt gct cag gag agg gga gat gtg atg gac ttc tat aaa acc	96
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr	
20 25 30	
cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg	144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu	
35 40 45	
gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat	192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp	
50 55 60	
ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa	240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys	
65 70 75 80	
gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa	288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys	
85 90 95	
gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt	336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu	
100 105 110	
tcc tcg ggg gaa aca gac tta aag ctt ttg gaa gaa agc att gca aac	384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn	
115 120 125	
ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc	432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser	
130 135 140	

act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac	480
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His	
145 150 155 160	
tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc	528
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr	
165 170 175	
aac ggt ggc aat gtg aaa ttg tat acc aca gac caa agc acc ttt gac	576
Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp	
180 185 190	
att ttg cag gat ttg gag ttt tct tct ggg tcc cca ggt aaa gag acg	624
Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr	
195 200 205	
aat gag agt cct tgg aga tca gac ctg ttg ata gat gaa aac tgt ttg	672
Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu	
210 215 220	
ctt tct cct ctg gcg gga gaa gac gat tca ttc ctt ttg gaa gga aac	720
Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn	
225 230 235 240	
tcg aat gag gac tgc aag cct ctc att tta ccg gac act aaa ccc aaa	768
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys	
245 250 255	
att aag gat aat gga gat ctg gtt ttg tca agc ccc agt aat gta aca	816
Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr	
260 265 270	
ctg ccc caa gtg aaa aca gaa aaa gaa gat ttc atc gaa ctc tgc acc	864
Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr	
275 280 285	
cct ggg gta att aag caa gag aaa ctg ggc aca gtt tac tgt cag gca	912
Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala	
290 295 300	
agc ttt cct gga gca aat ata att ggt aat aaa atg tct gcc att tct	960
Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser	
305 310 315 320	
gtt cat ggt gtg agt acc tct gga gga cag atg tac cac tat gac atg	1008
Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met	
325 330 335	
aat aca gca tcc ctt tct caa cag cag gat cag aag cct att ttt aat	1056
Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn	
340 345 350	

gtc att cca cca att ccc gtt ggt tcc gaa aat tgg aat agg tgc caa	1104
Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln	
355 360 365	
gga tct gga gat gac aac ttg act tct ctg ggg act ctg aac ttc cct	1152
Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro	
370 375 380	
ggt cga aca gtt ttt tct aat ggc tat tca agc ccc agc atg aga cca	1200
Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro	
385 390 395 400	
gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca	1248
Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro	
405 410 415	
cct ccc agc ggc cgc gtg caa gag gag ctg tgc ctg gtt tgc ggc gac	1296
Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp	
420 425 430	
agg gcc tcc ggc tac cac tac aac gcc ctc acc tgt gga tcc tgc aag	1344
Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys	
435 440 445	
gtg ttc ttt cga cgc agc gtt acg aag agc gcc gtc tac tgc tgc aag	1392
Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys	
450 455 460	
ttc ggg cgc gcc tgc gaa atg gac atg tac atg agg cga aag tgt cag	1440
Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln	
465 470 475 480	
gag tgc cgc ctg aaa aag tgc ctg gcc gtg ggt atg cgg ccg gaa tgc	1488
Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys	
485 490 495	
gtc gtc ccg gag aac caa tgt gcg atg aag cgg cgc gaa aag aag gcc	1536
Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala	
500 505 510	
cag aag gag aag gac aaa atg acc act tcg ccg agc tct cag cat ggc	1584
Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly	
515 520 525	
ggc aat ggc agc ttg gcc tct ggt ggc ggc caa gac ttt gtt aag aag	1632
Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys	
530 535 540	
gag att ctt gac ctt atg aca tgc gag ccg ccc cag cat gcc act att	1680
Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile	
545 550 555 560	

ccg cta cta cct gat gaa ata ttg gcc aag tgt caa gcg cgc aat ata	1728
Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile	
565 570 575	
cct tcc tta acg tac aat cag ttg gcc gtt ata tac aag tta att tgg	1776
Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp	
580 585 590	
tac cag gat ggc tat gag cag cca tct gaa gag gat ctc agg cgt ata	1824
Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile	
595 600 605	
atg agt caa ccc gat gag aac gag agc caa acg gac gtc agc ttt cgg	1872
Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg	
610 615 620	
cat ata acc gag ata acc ata ctc acg gtc cag ttg att gtt gag ttt	1920
His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe	
625 630 635 640	
gct aaa ggt cta cca gcg ttt aca aag ata ccc cag gag gac cag atc	1968
Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile	
645 650 655	
acg tta cta aag gcc tgc tcg tcg gag gtg atg atg ctg cgt atg gca	2016
Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala	
660 665 670	
cga cgc tat gac cac agc tcg gac tca ata ttc ttc gcg aat aat aga	2064
Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg	
675 680 685	
tca tat acg cgg gat tct tac aaa atg gcc gga atg gct gat aac att	2112
Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile	
690 695 700	
gaa gac ctg ctg cat ttc tgc cgc caa atg ttc tcg atg aag gtg gac	2160
Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp	
705 710 715 720	
aac gtc gaa tac gcg ctt ctc act gcc att gtg atc ttc tcg gac cgg	2208
Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg	
725 730 735	
ccg ggc ctg gag aag gcc caa cta gtc gaa gcg atc cag agc tac tac	2256
Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr	
740 745 750	
atc gac acg cta cgc att tat ata ctc aac cgc cac tgc ggc gac tca	2304
Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser	
755 760 765	

E

atg agc ctc gtc ttc tac gca aag ctg ctc tcg atc ctc acc gag ctg	2352
Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu	
770 775 780	
cg t acg ctg ggc aac cag aac gcc gag atg tgt ttc tca cta aag ctc	2400
Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu	
785 790 795 800	
aaa aac cgc aaa ctg ccc aag ttc ctc gag gag atc tgg gac gtt cat	2448
Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His	
805 810 815	
gcc atc ccg cca tcg gtc cag tcg cac ctt cag att acc cag gag gag	2496
Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu	
820 825 830	
aac gag cg t ctc gag cgg gct gag cg t atg cgg gca tcg gtt ggg ggc	2544
Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly	
835 840 845	
gcc att acc gcc ggc att gat tgc gac tct gcc tcc act tcg gcg gcg	2592
Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala	
850 855 860	
gca gcc gcg gcc cag cat cag cct cag cct cag ccc cag ccc caa ccc	2640
Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro	
865 870 875 880	
tcc tcc ctg acc cag aac gat tcc cag cac cag aca cag ccg cag cta	2688
Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu	
885 890 895	
caa cct cag cta cca cct cag ctg caa ggt caa ctg caa ccc cag ctc	2736
Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu	
900 905 910	
caa cca cag ctt cag acg caa ctc cag cca cag att caa cca cag cca	2784
Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro	
915 920 925	
cag ctc ctt ccc gtc tcc gct ccc gtg ccc gcc tcc gta acc gca cct	2832
Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro	
930 935 940	
ggt tcc ttg tcc gcg gtc agt acg agc agc gaa tac atg ggc gga agt	2880
Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser	
945 950 955 960	
gcg gcc ata gga ccc atc acg ccg gca acc acc agc agt atc acg gct	2928
Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala	
965 970 975	

gcc gtt acc gct agc tcc acc aca tca gcg gta ccg atg ggc aac gga 2976
 Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
 980 985 990

gtt gga gtc ggt gtt ggg gtg ggc ggc aac gtc agc atg tat gcg aac 3024
 Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
 995 1000 1005

gcc cag acg gcg atg gcc ttg atg ggt gta gcc ctg cat tcg cac caa 3072
 Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 1010 1015 1020

gag cag ctt atc ggg gga gtg gcg gtt aag tcg gag cac tcg acg act 3120
 Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 1025 1030 1035 1040

gca tag 3126
 Ala

<210> 9
 <211> 1041
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Recombinant
 GEcR

<400> 9
 Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
 1 5 10 15

Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 20 25 30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35 40 45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
 50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
 65 70 75 80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
 100 105 110



Ser	Ser	Gly	Glu	Thr	Asp	Leu	Lys	Leu	Leu	Glu	Glu	Ser	Ile	Ala	Asn	
		115					120					125				
Leu	Asn	Arg	Ser	Thr	Ser	Val	Pro	Glu	Asn	Pro	Lys	Ser	Ser	Ala	Ser	
	130					135					140					
Thr	Ala	Val	Ser	Ala	Ala	Pro	Thr	Glu	Lys	Glu	Phe	Pro	Lys	Thr	His	
145					150					155					160	
Ser	Asp	Val	Ser	Ser	Glu	Gln	Gln	His	Leu	Lys	Gly	Gln	Thr	Gly	Thr	
				165					170					175		
Asn	Gly	Gly	Asn	Val	Lys	Leu	Tyr	Thr	Thr	Asp	Gln	Ser	Thr	Phe	Asp	
			180					185					190			
Ile	Leu	Gln	Asp	Leu	Glu	Phe	Ser	Ser	Gly	Ser	Pro	Gly	Lys	Glu	Thr	
		195					200					205				
Asn	Glu	Ser	Pro	Trp	Arg	Ser	Asp	Leu	Leu	Ile	Asp	Glu	Asn	Cys	Leu	
	210					215					220					
Leu	Ser	Pro	Leu	Ala	Gly	Glu	Asp	Asp	Ser	Phe	Leu	Leu	Glu	Gly	Asn	
225					230					235					240	
Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys	
				245					250					255		
Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr	
			260					265					270			
Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr	
		275					280					285				
Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala	
	290					295					300					
Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser	
305					310					315					320	
Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met	
				325					330					335		
Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn	
			340					345					350			
Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln	
		355					360					365				
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro	
		370				375					380					

Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro	385	390	395	400
Asp	Val	Ser	Ser	Pro	Pro	Ser	Ser	Ser	Ser	Thr	Ala	Thr	Thr	Gly	Pro	405	410	415	
Pro	Pro	Ser	Gly	Arg	Val	Gln	Glu	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	420	425	430	
Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	435	440	445	
Val	Phe	Phe	Arg	Arg	Ser	Val	Thr	Lys	Ser	Ala	Val	Tyr	Cys	Cys	Lys	450	455	460	
Phe	Gly	Arg	Ala	Cys	Glu	Met	Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	465	470	475	480
Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	485	490	495	
Val	Val	Pro	Glu	Asn	Gln	Cys	Ala	Met	Lys	Arg	Arg	Glu	Lys	Lys	Ala	500	505	510	
Gln	Lys	Glu	Lys	Asp	Lys	Met	Thr	Thr	Ser	Pro	Ser	Ser	Gln	His	Gly	515	520	525	
Gly	Asn	Gly	Ser	Leu	Ala	Ser	Gly	Gly	Gly	Gln	Asp	Phe	Val	Lys	Lys	530	535	540	
Glu	Ile	Leu	Asp	Leu	Met	Thr	Cys	Glu	Pro	Pro	Gln	His	Ala	Thr	Ile	545	550	555	560
Pro	Leu	Leu	Pro	Asp	Glu	Ile	Leu	Ala	Lys	Cys	Gln	Ala	Arg	Asn	Ile	565	570	575	
Pro	Ser	Leu	Thr	Tyr	Asn	Gln	Leu	Ala	Val	Ile	Tyr	Lys	Leu	Ile	Trp	580	585	590	
Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Arg	Arg	Ile	595	600	605	
Met	Ser	Gln	Pro	Asp	Glu	Asn	Glu	Ser	Gln	Thr	Asp	Val	Ser	Phe	Arg	610	615	620	
His	Ile	Thr	Glu	Ile	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	625	630	635	640
Ala	Lys	Gly	Leu	Pro	Ala	Phe	Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	645	650	655	

Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	
			660					665					670			
Arg	Arg	Tyr	Asp	His	Ser	Ser	Asp	Ser	Ile	Phe	Phe	Ala	Asn	Asn	Arg	
		675					680					685				
Ser	Tyr	Thr	Arg	Asp	Ser	Tyr	Lys	Met	Ala	Gly	Met	Ala	Asp	Asn	Ile	
	690					695					700					
Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Gln	Met	Phe	Ser	Met	Lys	Val	Asp	
705					710					715					720	
Asn	Val	Glu	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	
				725					730					735		
Pro	Gly	Leu	Glu	Lys	Ala	Gln	Leu	Val	Glu	Ala	Ile	Gln	Ser	Tyr	Tyr	
			740					745					750			
Ile	Asp	Thr	Leu	Arg	Ile	Tyr	Ile	Leu	Asn	Arg	His	Cys	Gly	Asp	Ser	
		755					760					765				
Met	Ser	Leu	Val	Phe	Tyr	Ala	Lys	Leu	Leu	Ser	Ile	Leu	Thr	Glu	Leu	
	770					775					780					
Arg	Thr	Leu	Gly	Asn	Gln	Asn	Ala	Glu	Met	Cys	Phe	Ser	Leu	Lys	Leu	
785					790					795					800	
Lys	Asn	Arg	Lys	Leu	Pro	Lys	Phe	Leu	Glu	Glu	Ile	Trp	Asp	Val	His	
				805					810					815		
Ala	Ile	Pro	Pro	Ser	Val	Gln	Ser	His	Leu	Gln	Ile	Thr	Gln	Glu	Glu	
			820					825					830			
Asn	Glu	Arg	Leu	Glu	Arg	Ala	Glu	Arg	Met	Arg	Ala	Ser	Val	Gly	Gly	
	835						840					845				
Ala	Ile	Thr	Ala	Gly	Ile	Asp	Cys	Asp	Ser	Ala	Ser	Thr	Ser	Ala	Ala	
	850					855					860					
Ala	Ala	Ala	Ala	Gln	His	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	
865					870					875					880	
Ser	Ser	Leu	Thr	Gln	Asn	Asp	Ser	Gln	His	Gln	Thr	Gln	Pro	Gln	Leu	
				885					890					895		
Gln	Pro	Gln	Leu	Pro	Pro	Gln	Leu	Gln	Gly	Gln	Leu	Gln	Pro	Gln	Leu	
			900					905					910			
Gln	Pro	Gln	Leu	Gln	Thr	Gln	Leu	Gln	Pro	Gln	Ile	Gln	Pro	Gln	Pro	
			915				920					925				

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
980 985 990

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
1010 1015 1020

Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
1025 1030 1035 1040

Ala

<210> 10
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified
ecdysone response element

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (7)..(11)
<223> a, c, t, g, other or unknown, wherein the length of this
region may vary in length from 0 to 5, with 1 being
especially preferred

<220>
<221> modified_base
<222> (14)..(15)
<223> a, c, t, g, other or unknown

<400> 10
rgbnnmnnnn ntgnncy

17



<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified
ecdysone response element

<220>
<221> modified_base
<222> (3)..(4)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (7)..(11)
<223> a, c, t, g, other or unknown, wherein the length of this
region may vary in length from 0 to 5, with 1 being
especially preferred

<220>
<221> modified_base
<222> (13)..(14)
<223> a, c, t, g, other or unknown

<400> 11
rgnncannnn nknnvcy

17

<210> 12
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified
ecdysone response element

<220>
<221> modified_base
<222> (7)
<223> a, c, t, g, other or unknown

<400> 12
agtgcantgt tct

13

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified
ecdysone response element

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (7)..(11)
<223> a, c, t, g, other or unknown, wherein the length of this
region may vary in length from 0 to 5, with 3 being
especially preferred

<220>
<221> modified_base
<222> (15)..(16)
<223> a, c, t, g, other or unknown

<400> 13
rgbnnmnnnn nrgbnnm

17

<210> 14
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
tacaacgccc tcacctgtgg atcctgcaag gtgtttcttt cgacgcagc

49

<210> 15
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
gtactcccg ggcggggcta tgcggggcgg ggctaatacgc taggggcggg gca 53

<210> 16
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 16
gtactgcccc gccctagcg attagccccg ccccgcatag ccccgccccg gga 53

<210> 17
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 17
agctcgatgg acaagtgcac tgttctttgc tgaa 34

<210> 18
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18
agctttcagc aagagaacaa tgcacttgct catcg 35